

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/579,690
Source: TFWP
Date Processed by STIC: 05/31/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 05/31/2006

PATENT APPLICATION: US/10/579,690

TIME: 13:31:55

Input Set: E:\SEQUEST.txt

Output Set: N:\CRF4\05312006\J579690.raw

```

4 <110> APPLICANT: BASF AKTIENGESELLSCHAFT et al.
6 <120> TITLE OF INVENTION: METHODS FOR THE PREPARATION OF LYSINE BY
7   FERMENTATION OF CORYNEBACTERIUM GLUTAMICUM
10 <130> FILE REFERENCE: BGI-158PC2
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/579,690
C--> 13 <141> CURRENT FILING DATE: 2006-05-18
15 <150> PRIOR APPLICATION NUMBER: PCT/IB2003/006456
16 <151> PRIOR FILING DATE: 2003-12-18
18 <160> NUMBER OF SEQ ID NOS: 24
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1070
24 <212> TYPE: DNA
25 <213> ORGANISM: Corynebacterium glutamicum
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (22)...(1029)
31 <400> SEQUENCE: 1
32 gtgccccagg aggcccttca g atg aac cta aag aac ccc gaa acg cca gac 51
33                               Met Asn Leu Lys Asn Pro Glu Thr Pro Asp
34                               1           5           10
36 cgt aac ctt gct atg gag ctg gtg cga gtt acg gaa gca gct gca ctg 99
37 Arg Asn Leu Ala Met Glu Leu Val Arg Val Thr Glu Ala Ala Ala Leu
38           15           20           25
40 gct tct gga cgt tgg gtt gga cgt ggc atg aag aat gaa ggc gac ggt 147
41 Ala Ser Gly Arg Trp Val Gly Arg Gly Met Lys Asn Glu Gly Asp Gly
42           30           35           40
44 gcc gct gtt gac gcc atg cgc cag ctc atc aac tca gtg acc atg aag 195
45 Ala Ala Val Asp Ala Met Arg Gln Leu Ile Asn Ser Val Thr Met Lys
46           45           50           55
48 ggc gtc gtt gtt atc ggc gag ggc gaa aaa gac gaa gct cca atg ctg 243
49 Gly Val Val Val Ile Gly Glu Gly Glu Lys Asp Glu Ala Pro Met Leu
50           60           65           70
52 tac aac ggc gaa gag gtc gga acc ggc ttt gga cct gag gtt gat atc 291
53 Tyr Asn Gly Glu Glu Val Gly Thr Gly Phe Gly Pro Glu Val Asp Ile
54 75           80           85           90
56 gca gtt gac cca gtt gac ggc acc acc ctg atg gct gag ggt cgc ccc 339
57 Ala Val Asp Pro Val Asp Gly Thr Thr Leu Met Ala Glu Gly Arg Pro
58           95          100          105
60 aac gca att tcc att ctc gca gct gca gag cgt ggc acc atg tac gat 387
61 Asn Ala Ile Ser Ile Leu Ala Ala Glu Arg Gly Thr Met Tyr Asp
62          110          115          120
64 cca tcc tcc gtc ttc tac atg aag aag atc gcc gtg gga cct gag gcc 435

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65 Pro Ser Ser Val Phe Tyr Met Lys Lys Ile Ala Val Gly Pro Glu Ala
66      125      130      135
68 gca ggc aag atc gac atc gaa gct cca gtt gcc cac aac atc aac gcg 483
69 Ala Gly Lys Ile Asp Ile Glu Ala Pro Val Ala His Asn Ile Asn Ala
70      140      145      150
72 gtg gca aag tcc aag gga atc aac cct tcc gac gtc acc gtt gtc gtg 531
73 Val Ala Lys Ser Lys Gly Ile Asn Pro Ser Asp Val Thr Val Val Val
74 155      160      165      170
76 ctt gac cgt cct cgc cac atc gaa ctg atc gca gac att cgt cgt gca 579
77 Leu Asp Arg Pro Arg His Ile Glu Leu Ile Ala Asp Ile Arg Arg Ala
78      175      180      185
80 ggc gca aag gtt cgt ctc atc tcc gac ggc gac gtt gca ggt gca gtt 627
81 Gly Ala Lys Val Arg Leu Ile Ser Asp Gly Asp Val Ala Gly Ala Val
82      190      195      200
84 gca gca gct cag gat tcc aac tcc gtg gac atc atg atg ggc acc ggc 675
85 Ala Ala Ala Gln Asp Ser Asn Ser Val Asp Ile Met Met Gly Thr Gly
86      205      210      215
88 gga acc cca gaa ggc atc atc act gcg tgc gcc atg aag tgc atg ggt 723
89 Gly Thr Pro Glu Gly Ile Ile Thr Ala Cys Ala Met Lys Cys Met Gly
90      220      225      230
92 ggc gaa atc cag ggc atc ctg gcc cca atg aac gat ttc gag cgc cag 771
93 Gly Glu Ile Gln Gly Ile Leu Ala Pro Met Asn Asp Phe Glu Arg Gln
94 235      240      245      250
96 aag gca cac gac gct ggt ctg gtt ctt gat cag gtt ctg cac acc aac 819
97 Lys Ala His Asp Ala Gly Leu Val Leu Asp Gln Val Leu His Thr Asn
98      255      260      265
100 gat ctg gtg agc tcc gac aac tgc tac ttc gtg gca acc ggt gtg acc 867
101 Asp Leu Val Ser Ser Asp Asn Cys Tyr Phe Val Ala Thr Gly Val Thr
102      270      275      280
104 aac ggt gac atg ctc cgt ggc gtt tcc tac cgc gca aac ggc gca acc 915
105 Asn Gly Asp Met Leu Arg Gly Val Ser Tyr Arg Ala Asn Gly Ala Thr
106      285      290      295
108 acc cgt tcc ctg gtt atg cgc gca aag tca ggc acc atc cgc cac atc 963
109 Thr Arg Ser Leu Val Met Arg Ala Lys Ser Gly Thr Ile Arg His Ile
110      300      305      310
112 gag tct gtc cac cag ctg tcc aag ctg cag gaa tac tcc gtg gtt gac 1011
113 Glu Ser Val His Gln Leu Ser Lys Leu Gln Glu Tyr Ser Val Val Asp
114 315      320      325      330
116 tac acc acc gcg acc taa gagctcttag ttcgaaaaaac cgccggccat 1059
117 Tyr Thr Thr Ala Thr *
118      335
120 tgtgggtcggc g 1070
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 335
124 <212> TYPE: PRT
125 <213> ORGANISM: Corynebacterium glutamicum
127 <400> SEQUENCE: 2
128 Met Asn Leu Lys Asn Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu
129 1 5 10 15

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130 Leu Val Arg Val Thr Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val
131      20      25      30
132 Gly Arg Gly Met Lys Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met
133      35      40      45
134 Arg Gln Leu Ile Asn Ser Val Thr Met Lys Gly Val Val Val Ile Gly
135      50      55      60
136 Glu Gly Glu Lys Asp Glu Ala Pro Met Leu Tyr Asn Gly Glu Glu Val
137 65      70      75      80
138 Gly Thr Gly Phe Gly Pro Glu Val Asp Ile Ala Val Asp Pro Val Asp
139      85      90      95
140 Gly Thr Thr Leu Met Ala Glu Gly Arg Pro Asn Ala Ile Ser Ile Leu
141      100     105     110
142 Ala Ala Ala Glu Arg Gly Thr Met Tyr Asp Pro Ser Ser Val Phe Tyr
143      115     120     125
144 Met Lys Lys Ile Ala Val Gly Pro Glu Ala Ala Gly Lys Ile Asp Ile
145      130     135     140
146 Glu Ala Pro Val Ala His Asn Ile Asn Ala Val Ala Lys Ser Lys Gly
147 145     150     155     160
148 Ile Asn Pro Ser Asp Val Thr Val Val Val Leu Asp Arg Pro Arg His
149      165     170     175
150 Ile Glu Leu Ile Ala Asp Ile Arg Arg Ala Gly Ala Lys Val Arg Leu
151      180     185     190
152 Ile Ser Asp Gly Asp Val Ala Gly Ala Val Ala Ala Ala Gln Asp Ser
153      195     200     205
154 Asn Ser Val Asp Ile Met Met Gly Thr Gly Gly Thr Pro Glu Gly Ile
155      210     215     220
156 Ile Thr Ala Cys Ala Met Lys Cys Met Gly Gly Glu Ile Gln Gly Ile
157 225     230     235     240
158 Leu Ala Pro Met Asn Asp Phe Glu Arg Gln Lys Ala His Asp Ala Gly
159      245     250     255
160 Leu Val Leu Asp Gln Val Leu His Thr Asn Asp Leu Val Ser Ser Asp
161      260     265     270
162 Asn Cys Tyr Phe Val Ala Thr Gly Val Thr Asn Gly Asp Met Leu Arg
163      275     280     285
164 Gly Val Ser Tyr Arg Ala Asn Gly Ala Thr Thr Arg Ser Leu Val Met
165      290     295     300
166 Arg Ala Lys Ser Gly Thr Ile Arg His Ile Glu Ser Val His Gln Leu
167 305     310     315     320
168 Ser Lys Leu Gln Glu Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
169      325     330     335
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 35
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Synthetic construct
180 <400> SEQUENCE: 3
181 gagagagaga cgcgtcccag tggctgagac gcatac
183 <210> SEQ ID NO: 4

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184 <211> LENGTH: 34
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: Synthetic construct
191 <400> SEQUENCE: 4
192 ctctctctgt cgacgaattc aatcttacgg cctg          34
194 <210> SEQ ID NO: 5
195 <211> LENGTH: 4323
196 <212> TYPE: DNA
197 <213> ORGANISM: Corynebacterium glutamicum
199 <400> SEQUENCE: 5
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201 tatcgtcgac atcgatgctc ttctgcgtta attaacaatt gggatcctct agaccgagg 120
202 tttaaatcgc tagcgggctg ctaaagggaag cggaacacgt agaaagccag tccgcagaaa 180
203 cgggtgctgac cccggatgaa tgtcagctac tgggctatct ggacaaggga aaacgcaagc 240
204 gcaaagagaa agcaggtagc ttgcagtggg cttacatggc gatagctaga ctgggcgggt 300
205 ttatggacag caagcgaacc ggaattgcc a gctggggcgc cctctggtaa gggtgggaag 360
206 cctgcaaag taaactggat ggctttcttg ccgccaagg tctgatggcg caggggatca 420
207 agatctgac aagagacagg atgaggatcg ttctgcata ttgaacaaga tggattgcac 480
208 gcaggttctc cggccgcttg ggtggagagg ctattcggct atgactgggc acaacagaca 540
209 atcggctgct ctgatccgc cgtgttcgg ctgtcagcgc aggggcgccc gggtcttttt 600
210 gtcaagaccg acctgtccgg tgccctgaat gaactgcagg acgaggcagc gcggctatcg 660
211 tggctggcca cgacgggctg tccttgcgca gctgtgctcg acgttgtcac tgaagcggga 720
212 agggactggc tgctattggg cgaagtgcg gggcaggatc tcctgtcatc tcaccttgct 780
213 cctgccgaga aagtatccat catggctgat gcaatgcggc ggctgcatac gcttgatccg 840
214 gctacctgcc cattcgacca ccaagcgaac catcgcatcg agcagacag tactcggatg 900
215 gaagccggtc ttgtcgatca ggatgatctg gacgaagagc atcaggggct cgcgccagcc 960
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218 tgtggccggc tgggtgtggc ggaccgctat caggacatag cgttggctac ccgtgatatt 1140
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220 cccgattcgc agcgcacgc cttctatcgc cttcttgacg agttcttctg agcgggactc 1260
221 tggggttcga aatgaccgac caagcgacgc ccaacctgcc atcacgagat ttcgattcca 1320
222 ccgcgcctt ctatgaaagg ttgggcttcg gaatcgtttt ccgggacgcc ggctggatga 1380
223 tcctccagcg cggggatctc atgctggagt tcttcgcca cgctagcggc gcgcgggccc 1440
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227 tgagcaaaaag gccagcaaaa ggccaggaac cgtaaaaagg ccgcgttgct ggcgtttttc 1680
228 cataggctcc gccccctga cgagcatcac aaaaatcgac gctcaagtca gaggtggcga 1740
229 aacccgacag gactataaag ataccaggcg ttccccctg gaagctccct cgtgcgctct 1800
230 cctgttcoga cctgcgct taccggatac ctgtccgctt ttctcccttc gggaagcgtg 1860
231 gcgctttctc atagctcacg ctgtaggtat ctacgttcgg ttaggtcgt tcgctccaag 1920
232 ctgggctgtg tgcacgaacc cccggttcag cccgaccgct gcgccttatc cggtaactat 1980
233 cgtcttgagt ccaacccggt aagacacgac ttatcgccac tggcagcagc cactggtaac 2040
234 aggattagca gacgaggtta tgtaggcggt gctacagagt tcttgaagtg gtggcctaac 2100
235 tacggctaca ctagaaggac agtatattgg atctgcgctc tgctgaagcc agttaccttc 2160
236 ggaaaaagag ttggtagctc ttgatccggc aaacaaacca ccgctggtag cggtggtttt 2220

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237 tttgtttgca agcagcagat tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc 2280
238 ttttctacgg ggtctgacgc tcagtggaac gaaaactcac gttaagggat tttggtcatg 2340
239 agattatcaa aaaggatcct cacctagatc cttttaagg ccggccgcgg ccgccatcgg 2400
240 cattttcttt tgcgttttta tttgttaact gttaattgtc cttgttcaag gatgctgtct 2460
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243 ttcgcttgag gtacagcga gtgtgagtaa gtaaaggtta catcgttagg atcaagatcc 2640
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245 acataaccaa gcatgtaaat atcgtttagc gtaatgccgt caatcgtcac ttttgatccg 2760
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247 tcatctgtta ctgtgttaga tgcaatcagc ggtttcatca cttttttcag tgtgtaatca 2880
248 tcgttttagc caatcatacc gagagcgcgg tttgctaact cagccgtgcg ttttttatcg 2940
249 ctttgcagaa gtttttgact ttcttgacgg aagaatgatg tgcttttgcc atagtatgct 3000
250 ttgttaaata aagattcttc gccttggtag ccattctcag ttccagtgtt tgcttcaaat 3060
251 actaagtatt tgtggccttt atcttctacg tagtgaggat ctctcagcgt atggttgctg 3120
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253 ccgtcaaaga ttgatttata atcctctaca ccgttgatgt tcaaagagct gtctgatgct 3240
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255 gtgtagaata atcggatttt tccgtcagat gtaaatgtgg ctgaacctga ccatctctg 3360
256 gtttggtctt ttaggataga atcatttgca tcgaatttgt cgtgtcttt aaagacgcgg 3420
257 ccagcgtttt tccagctgtc aatagaagtt tcgccgactt tttgatagaa catgtaaatc 3480
258 gatgtgtcat ccgcattttt aggatctccg gctaattgcaa agacgatgtg gtagccgtga 3540
259 tagtttgcaa cagtgccgtc agcgttttgt aatggccagc tgtcccaaac gtccaggcct 3600
260 tttgcagaag agatattttt aattgtggac gaatcaaatt cagaaacttg atatttttca 3660
261 tttttttgct gttcagggat ttgcagcata tcatggcgtg taatatggga aatgccgtat 3720
262 gtttccttat atggcttttg gttcgtttct ttcgcaaacg cttgagttgc gcctcctgcc 3780
263 agcagtgcgg tagtaaagggt taatactgtt gcttgtttg caaacttttt gatgttcac 3840
264 gttcatgtct ctttttttat gtactgtgtt agcgtgtgc ttcttcagc cctcctgttt 3900
265 gaagatggca agtttagttac gcacaataaa aaaagacctt aaatatgtaa ggggtgacgc 3960
266 caaagtatac actttgcctt ttacacattt taggtcttgc ctgctttatc agtaacaaac 4020
267 ccgcgcgatt tacttttcga cctcattcta ttagactctc gtttggtatt caactggctc 4080
268 attttcctct tttgtttgat agaaaatcat aaaaggattt gcagactacg ggcctaaaga 4140
269 actaaaaaat ctatctgttt cttttcattc tctgtatttt ttatagtttc tgttgcatgg 4200
270 gcataaagtt gcctttttta tcacaattca gaaaatatca taatatctca tttcactaaa 4260
271 taatagttaa cggcaggtat atgtgatggg ttaaaaagga tcggcgccgg ctcgatttaa 4320
272 atc 4323

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274 <210> SEQ ID NO: 6

275 <211> LENGTH: 5860

276 <212> TYPE: DNA

277 <213> ORGANISM: Corynebacterium glutamicum

279 <400> SEQUENCE: 6

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280 cccggtacca cgcgtcccag tggctgagac gcatccgcta aagccccagg aaccctgtgc 60
281 agaaagaaaa cactcctctg gctaggtaga cacagtttat aaaggtagag ttgagcgggt 120
282 aactgtcagc acgtagatcg aaagggtcac aaagggtggc ctggtcgtac agaaatatgg 180
283 cgttccctcg cttgagagtg cggaacgcat tagaaacgtc gctgaacgga tcgttgccac 240
284 caagaaggct ggaaatgatg tcgtggttgt ctgctccgca atgggagaca ccacggatga 300
285 acttctagaa cttgcagcgg cagtgaatcc cgttccgcca gctcgtgaaa tggatatgct 360
286 cctgactgct ggtgagcgtg tttctaacgc tctcgtcgcc atggctattg agtccttgg 420
287 cgcagaagcc caatctttca cgggctctca ggctggtgtg ctcaccaccg agcgccacgg 480

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date